

## EXHIBIT A

Docket No.: PF-0619 USN  
USSN: 09/807,452**SeqServer**  
biology in silico**BLAST2 Search Results**

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

GCG Assembly

Phrap

Translation

BLAST2 Manual

Confidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: **blastp**

Sequence ID(s):

☐ 4325626CD1 vs. genpept136

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 4325626CD1  
(549 letters)

Database: genpept136  
1,453,555 sequences; 449,659,834 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<input checked="" type="checkbox"/> <u>g23452665</u> Rab GTPase-activating protein PRC17 [Homo sapiens]	1164	0.0
<input checked="" type="checkbox"/> <u>g12053225</u> hypothetical protein [Homo sapiens]	1160	0.0
<input checked="" type="checkbox"/> <u>g37330</u> oncogene [Homo sapiens]	855	0.0
<input checked="" type="checkbox"/> <u>g24474450</u> ubiquitin-specific protease USP6 [Homo sapiens]	854	0.0
<input checked="" type="checkbox"/> <u>g37333</u> oncogene [Homo sapiens]	602	e-171
<input checked="" type="checkbox"/> <u>g37334</u> oncogene [Homo sapiens]	257	4e-67
<input checked="" type="checkbox"/> <u>g29881565</u> Expressed sequence AI316785 [Mus musculus]	250	9e-65
<input checked="" type="checkbox"/> <u>g27695568</u> related to the N terminus of tre [Homo sapiens]	245	2e-63
<input checked="" type="checkbox"/> <u>g2104571</u> KIAA0019 protein [Homo sapiens]	245	2e-63
<input checked="" type="checkbox"/> <u>g28703740</u> Hypothetical protein MGC51025 [Homo sapiens]	235	2e-60

>g23452665 Rab GTPase-activating protein PRC17 [Homo sapiens]  
Length = 549

Score = 1164 bits (2978), Expect = 0.0  
Identities = 548/549 (99%), Positives = 548/549 (99%)

Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60

Sbjct: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60  
MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60

Query: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120  
TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLN EEM  
Sbjct: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNIEEM 120

Query: 121 KLKNPGRYQIMKEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY 180  
KLKNPGRYQIMKEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY  
Sbjct: 121 KLKNPGRYQIMKEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY 180

Query: 181 NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE 240  
NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE  
Sbjct: 181 NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE 240

Query: 241 HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300  
HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI  
Sbjct: 241 HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300

Query: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP PP 360  
TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP PP  
Sbjct: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP PP 360

Query: 361 AKPEQGSSASRPVPASRGGKTLC KGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA 420  
AKPEQGSSASRPVPASRGGKTLC KGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA  
Sbjct: 361 AKPEQGSSASRPVPASRGGKTLC KGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA 420

Query: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV 480  
VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV  
Sbjct: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV 480

Query: 481 RAISQEDQLAPCWQAEP AERVRSFAAAPSTDSQGT PFRARDEQPCAPTS GPCLCGLHL 540  
RAISQEDQLAPCWQAEP AERVRSFAAAPSTDSQGT PFRARDEQPCAPTS GPCLCGLHL  
Sbjct: 481 RAISQEDQLAPCWQAEP AERVRSFAAAPSTDSQGT PFRARDEQPCAPTS GPCLCGLHL 540

Query: 541 ESSQFP PGF 549  
ESSQFP PGF  
Sbjct: 541 ESSQFP PGF 549

>g12053225 hypothetical protein [Homo sapiens]  
Length = 549

Score = 1160 bits (2969), Expect = 0.0

Identities = 546/549 (99%), Positives = 548/549 (99%)

Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60  
MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL  
Sbjct: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60

Query: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120  
TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM  
Sbjct: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120

Query: 121 KLKNPGRYQIMKEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY 180  
KLKNPGRYQIMKEKGK+SSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY  
Sbjct: 121 KLKNPGRYQIMKEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEY 180

Query: 181 NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE 240  
NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE  
Sbjct: 181 NPEVG YCRDL SHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGT VQGLQDQQE 240

Query: 241 HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300  
HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI  
Sbjct: 241 HVVATSQPKTMGHQDKKDL CGQCSPLGCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300

Query: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP 360  
TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRK+GDLPPP  
Sbjct: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKKGDLPPP 360

Query: 361 AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA 420  
AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA  
Sbjct: 361 AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA 420

Query: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV 480  
VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV  
Sbjct: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV 480

Query: 481 RAISQEDQLAPCWQAEHPAERVRSFAAAPSTSDQGTFFRARDEQPCAPTS GPCLCGLHL 540  
RAISQEDQLAPCWQAEHPAERVRSFAAAPSTSDQGTFFRARDEQ CAPTS GPCLCGLHL  
Sbjct: 481 RAISQEDQLAPCWQAEHPAERVRSFAAAPSTSDQGTFFRARDEQQCAPTS GPCLCGLHL 540

Query: 541 ESSQFPPGF 549  
ESSQFPPGF  
Sbjct: 541 ESSQFPPGF 549

>g37330 oncogene [Homo sapiens]  
Length = 786

Score = 855 bits (2185), Expect = 0.0

Identities = 407/500 (81%), Positives = 440/500 (87%), Gaps = 1/500 (0%)

Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVNDHLGIVHETELPPL 60  
MD+VE A S AQER+DI+MKY+KGHRAGLPEDKGP+P N+++D GI+HETELPP+  
Sbjct: 1 MDMVENADSLQAQERKDILMKYDKGHRAGLPEDKGPEPV-GINSSIDRFILHETELPPV 59

Query: 61 TAREAKQIRREISRSKSWVDMLGDWEKYKSSRKLIDRAYKGMMPNIRGPMWSVLLNTEEM 120  
TAREAK+IRRE++R SKW++MLG+WE YK S KLIDR YKG+PMNIRGP+WSVLLN +E+  
Sbjct: 60 TAREAKKIRREMTRTSKWMEMLGEWETYKHSSKLIDRVYKGIPMNIRGPVWSVLLNIQEI 119

Query: 121 KLKNPGRYQIMKEGKRSSEHIQIRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEY 180  
KLKNPGRYQIMKE+GKRSSEHI ID DV TLR H+FFRDRYG KQREL +ILLAY EY  
Sbjct: 120 KLKNPGRYQIMKERGKRSSEHIHHIDLDRVTTLRNHVFFRDRYGAKQRELFYILLAYSEY 179

Query: 181 NPEVGYCRDLSHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVQGLQDQQE 240  
NPEVGYCRDLSHI ALFLLYLPEEDAFWALVQLLASERHSL GFHSPNGGTVQGLQDQQE  
Sbjct: 180 NPEVGYCRDLSHITALFLLYLPEEDAFWALVQLLASERHSLPGFHSPNGGTVQGLQDQQE 239

Query: 241 HVVATSQPKTMGHQDKKDLGQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300  
HVV SQPKTM HQDK+ LCGQC+ LGCL+R LIDGISLGLTLRLWDVYLVEGEQ LMPI  
Sbjct: 240 HVVPSQPKTMWHQDKEGLCGQCASLGCLLRNLIDGISLGLTLRLWDVYLVEGEQVLMPI 299

Query: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP 360  
T IA KVQKRL KTSRCG WAR N+F DTWA ++DTVLKHLRAS KKLTRKQGDLP  
Sbjct: 300 TSIALKVQKRLMKTSRCGLWARLRNQFFDTWAMNDDTVLKHLRASTKKLTRKQGDLP 359

Query: 361 AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGA 420  
AK EQGS A RPVPASRGGKTLCKG RQAPPGPPA+F RPI SASPP A R STPCPGGA  
Sbjct: 360 AKREQGS LAPRPVPASRGGKTLCKGYRQAPPGPPAQFQRPIC SASPPWASRFSTPCPGGA 419

Query: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRHYDFRQSCWV 480  
VREDTYPVGTQGVPS ALAQGGPQGSWRFL+W SMPRLPTDLD+ GPWF HYDF +SCWV  
Sbjct: 420 VREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSMPRLPTDLDIGGPWFPHYDFERSCWV 479

Query: 481 RAISQEDQLAPCWQAEHPAE 500  
RAISQEDQLA CWQAEH E  
Sbjct: 480 RAISQEDQLATCWQAEHCGE 499

>g24474450 ubiquitin-specific protease USP6 [Homo sapiens]  
Length = 1406

Score = 854 bits (2182), Expect = 0.0

Identities = 407/500 (81%), Positives = 439/500 (87%), Gaps = 1/500 (0%)

Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60  
MD+VE A S AQER+DI+MKY+KGRAGLPEDKGP+P N+++D GI+HETELPP+  
Sbjct: 1 MDMVENADSLQAQERKDILMKYDKGHRAGLPEDKGPEPV-GINSSIDRFGILHETELPPV 59

Query: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120  
TAREAK+IRRE++R SKW++MLG+WE YK S KLIDR YKG+PMNIRGP+WSVLLN +E+  
Sbjct: 60 TAREAKKIRREMTRTSKWMEMLGEWETYKHSSKLIDRVYKGIPMNIRGPVWSVLLNIQEI 119

Query: 121 KLKNPGRYQIMKEGKRSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEY 180  
KLKNPGRYQIMKE+GKRSEHI ID DV TLR H+FFRDRYG KQREL +ILLAY EY  
Sbjct: 120 KLKNPGRYQIMKERGKRSEHIHHIDLDVRTTLRNHVFFRDRYGAKQRELFYILLAYSEY 179

Query: 181 NPEVGYCRDLSHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVQGLQDQQE 240  
NPEVGYCRDLSHI ALFLLYLPEEDAFWALVQLLASERHSL GFHSPNGGTVQGLQDQQE  
Sbjct: 180 NPEVGYCRDLSHITALFLLYLPEEDAFWALVQLLASERHSLPGFHSPNGGTVQGLQDQQE 239

Query: 241 HVVATSQPKTMGHQDKKDLGQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300  
HVV SQPKTM HQDK+ LCGQC+ LGCL+R LIDGISLGLTLRLWDVYLVEGEQ LMPI  
Sbjct: 240 HVVPSQPKTMWHQDKGLGQCASLGCLLRNLIDGISLGLTLRLWDVYLVEGEQVLMPI 299

Query: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP 360  
T IA KVQKRL KTSRCG WAR N+F DTWA ++DTVLKHLRAS KKLTRKQGDLP  
Sbjct: 300 TSIALKVQKRLMKTSRCGLWARLRNQFFDTWAMNDDTVLKHLRASTKKLTRKQGDLP 359

Query: 361 AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPAPRFPRIWSASPPRAPRSSTPCPGGA 420  
AK EQGS A RPVPASRGGKTLCKG RQAPPGPPA+F RPI SASPP A R STPCPGGA  
Sbjct: 360 AKREQGSLAPRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRFSTPCPGGA 419

Query: 421 VREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDL DVEGPWFRHYDFRQSCWV 480  
VREDTYPVGTQGVPS ALAQGGPQGSWRFL+W SMPRLPTDL D+ GPWF HYDF SCWV  
Sbjct: 420 VREDTYPVGTQGVPSLALAQGGPQGSWRFLQWNSMPRLPTDL DIGGPWFPHYDFEWSCWV 479

Query: 481 RAISQEDQLAPCWQAEHPAE 500  
RAISQEDQLA CWQAEH E  
Sbjct: 480 RAISQEDQLATCWQAEHCGE 499

>g37333 oncogene [Homo sapiens]  
Length = 376

Score = 602 bits (1536), Expect = e-171

Identities = 289/366 (78%), Positives = 318/366 (85%), Gaps = 1/366 (0%)

Query: 1 MDVVEVAGSWWAQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPL 60  
MD+VE A S AQER+DI+MKY+KGRAGLPEDKGP+P N+++D GI+HETELPP+  
Sbjct: 1 MDMVENADSLQAQERKDILMKYDKGHRAGLPEDKGPEPV-GINSSIDRFGILHETELPPV 59

Query: 61 TAREAKQIRREISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEM 120  
TAREAK+IRRE++R SKW++MLG+WE YK S KLIDR YKG+PMNIRGP+WSVLLN +E+  
Sbjct: 60 TAREAKKIRREMTRTSKWMEMLGEWETYKHSSKLIDRVYKGIPMNIRGPVWSVLLNIQEI 119

Query: 121 KLKNPGRYQIMKEGKRSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEY 180  
KLKNPGRYQIMKE+GKRSEHI ID DV TLR H+FFRDRYG KQREL +ILLAY EY  
Sbjct: 120 KLKNPGRYQIMKERGKRSEHIHHIDLDVRTTLRNHVFFRDRYGAKQRELFYILLAYSEY 179

Query: 181 NPEVGYCRDLSHIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVQGLQDQQE 240  
NPEVGYCRDLSHI ALFLLYLPEEDAFWALVQLLASERHSL GFHSPNGGTVQGLQDQQE  
Sbjct: 180 NPEVGYCRDLSHITALFLLYLPEEDAFWALVQLLASERHSLPGFHSPNGGTVQGLQDQQE 239

Query: 241 HVVATSQPKTMGHQDKKDLGQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPI 300  
HVV SQPKTM HQDK+ LCGQC+ LGCL+R LIDGISLGLTLRLWDVYLVEGEQ LMPI  
Sbjct: 240 HVVPKSQPKTMWHQDKGLCGQCASLGCLLRNLIDGISLGLTLRLWDVYLVEGEQVLMPI 299

Query: 301 TRIAFKVQKRLTKTSRCGPWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGDLP 360  
T IA KVQKRL KTSRCG WAR N+F DTWA ++DTVLKHLRAS KKLTRKQGDLP  
Sbjct: 300 TSIALKVQKRLMKTSRCGLWARLRNQFFDTWAMNDDTVLKHLRASTKKLTRKQGDLP 359

Query: 361 AKPEQG 366  
G  
Sbjct: 360 GPTALG 365

>g37334 oncogene [Homo sapiens]  
Length = 1089

Score = 257 bits (651), Expect = 4e-67  
Identities = 121/149 (81%), Positives = 125/149 (83%)

Query: 352 RKQGDLP 366 AKPEQGSSASRPVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPR 411  
R D AK EQGS A RPVPASRGGKTLCKG RQAPPGPPA+F RPI SASPP A R  
Sbjct: 34 RDPKDSRDAAKREQGSLAPRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASR 93

Query: 412 SSTPCPGGAVREDTYPVGTQGVPSPALAQGGPQGSWRFLQWNSMPRLPTDLDVEGPWFRH 471  
STPCPGGAVREDTYPVGTQGVPS ALAQGGPQGSWRFL+W SMPRLPTDLD+ GPWF H  
Sbjct: 94 FSTPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLQWNSMPRLPTDLDIGGPWFPH 153

Query: 472 YDFRQSCWVRAISQEDQLAPCWQAHPAE 500  
YDF +SCWVRAISQEDQLA CWQAHP E  
Sbjct: 154 YDFERSCWVRAISQEDQLATCWQAHCHE 182

>g29881565 Expressed sequence AI316785 [Mus musculus]  
Length = 707

Score = 250 bits (631), Expect = 9e-65  
Identities = 151/445 (33%), Positives = 223/445 (49%), Gaps = 18/445 (4%)

Query: 12 AQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPLTAREAKQIRRE 71  
AQER +I+ KY++G E + Y D G +HE ELP A +Q + E  
Sbjct: 35 AQERAEIVAKYDRGREGAEIEPWEDADYLVYKVT-DRFGFLHEEELPYHNAAADRQKQLE 93

Query: 72 ISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEMKLKNPGRYQIM 131  
I R SKW+ ML WE+YK++ K R YKG+P+ +RG +W++LL +MK + Y +  
Sbjct: 94 IERTSKWLKMLKKWERYKNTEKFHRRYKGIPLQLRGEVWALLLEIPKMKEETRDLYSKL 153

Query: 132 KEKGRSSEHIQRIDRDVSGTLRKHIFFRDRYGTQRELLHILLAYEYENPEVGYCRDLS 191  
K + + S I++ID DV+ T R HI FRDRYG KQ+ L H+L AY YN EVGYC+ +S  
Sbjct: 154 KHRARGCSPDIRQIDLDVNRTFRDHIMFRDRYGVKQQLFHVLAAYSINTEVGYCQGM 213

Query: 192 HIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVQGLQDQQEHVATSQPKTM 251  
I AL L+Y+ EEDAFWALV+L + +H++ GF + Q+ E ++ K  
Sbjct: 214 QITALLLMYMNEDAFWALVKLFSGPKHAMHGFVQGF PKLLRFQEHHEKILNKFLSKLK 273

Query: 252 GHQDKKDLGQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPITRIAFKVQK 311  
H D +++ + + +D L LR+WD+Y+ EGE+ L ++ K+ +K  
Sbjct: 274 QHLDSQEIIYTSFYTMKWFFQCFLDRTPFRLNLRWDIYIFEGERVLTAMSYTILKLHKKH 333

Query: 312 LTKTSRCGPWARFCNRFVDTWARD-----EDTVLKHLRASMKKLTRKQGDLP 365  
L K S +T A+D +D V++ L+ SM +L R + DLP P K ++  
Sbjct: 334 LMKLS---MEELVEFLQETLAKDFFEDDFVIEQLQVSMALKRAKLDLPEPGKEDEYP 389

Query: 366 GSSASRPVPASRGGKTLCKGDRQ-APPGPPAR-----FPRPIWSASPPRAPRSSTPCPG 418  
+ P S L G R P P PR SP R+ TP  
Sbjct: 390 KKPLGQLPPESACVNHLNNGQSVGRSPKTSRRREDGSPRKNHEHSPVHHSRNGTPERA 449

Query: 419 GAVREDTYPVGTQGVSPALAQGGP 443  
G R + G++ + A+Q P  
Sbjct: 450 GQSRKSVDEGSKNLKHEAESQRKP 474

>g27695568 related to the N terminus of tre [Homo sapiens]  
Length = 828

Score = 245 bits (620), Expect = 2e-63  
Identities = 148/434 (34%), Positives = 215/434 (49%), Gaps = 25/434 (5%)

Query: 12 AQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPLTAREAKQIRRE 71  
AQER +I+ KY++G E + Y D G +HE ELP +Q E  
Sbjct: 12 AQERAEIVAKYDRGREGAEIEPWEDADYLVYKVT-DRFGFLHEEELPDHNAVERQKHLE 70

Query: 72 ISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEMKLKNPGRYQIM 131  
I R +KW+ ML WEKYK++ K R YKG+P+ +RG +W++LL +MK + Y +  
Sbjct: 71 IERTTKWLKMLKGWEKYKNTEKFHRRYKGIPLQLRGEVWALLLEIPKMKEETRDLYSKL 130

Query: 132 KEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEYNPEVGYCRDLS 191  
K + + S I++ID DV+ T R HI FRDRYG KQ+ L H+L AY YN EVGYC+ +S  
Sbjct: 131 KHRARGCSPDIRQIDLDVNRTFRDHIMFRDRYGVKQQLFHVLAAYSIYNTEVGYCQGMS 190

Query: 192 HIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVOQLDQDQEHVVATSQPKTM 251  
I AL L+Y+ EEDAFWALV+L + +H++ GF + Q+ E ++ K  
Sbjct: 191 QITALLMYMNEEDAFWALVKLFSGPKHAMHGFFVQGFPKLLRFQEHHEKILNKFLSKLK 250

Query: 252 GHQDKKDLGCQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPITRIAFKVQQKR 311  
H D +++ + + +D L LR+WD+Y+ EGE+ L ++ K+ +K  
Sbjct: 251 QHLDSQEIIYTSFYTMKWFFQCFLDRTPTLNLRIWDIYIFEGERVLTAMSYTILKLHKKH 310

Query: 312 LTKTSRCGPWARFCNRFVDTWARD-----EDTVLKHRLASMKKLTRKQGDLPKPAK----P 363  
L K S F +T A+D +D V++ L+ SM +L R + DLP P K P  
Sbjct: 311 LMKLS----MEELVEFFQETLAKDFFEDDFVIEQLQISMTELKRAKLDLPEPGKEDEYP 366

Query: 364 EQGSSASRPVPASRGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGAVRE 423  
++ P S G L G R G P SP + R + P  
Sbjct: 367 KKPLGQLPPELQSWGVLHLSNGQRSV--GRP-----SPLASGRRESGAPHRHEH 414

Query: 424 DTYPVGTQGVSPA 437  
+P G P A  
Sbjct: 415 SPHPQSRTGTPERA 428

>g2104571 KIAA0019 protein [Homo sapiens]  
Length = 828

Score = 245 bits (620), Expect = 2e-63  
Identities = 148/434 (34%), Positives = 215/434 (49%), Gaps = 25/434 (5%)

Query: 12 AQEREDIIMKYEKGHRAGLPEDKGPKPFRSYNNNVVDHLGIVHETELPPLTAREAKQIRRE 71  
AQER +I+ KY++G E + Y D G +HE ELP +Q E  
Sbjct: 12 AQERAEIVAKYDRGREGAEIEPWEDADYLVYKVT-DRFGFLHEEELPDHNAVERQKHLE 70

Query: 72 ISRKSKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEMKLKNPGRYQIM 131  
I R +KW+ ML WEKYK++ K R YKG+P+ +RG +W++LL +MK + Y +  
Sbjct: 71 IERTTKWLKMLKGWEKYKNTEKFHRRYKGIPLQLRGEVWALLLEIPKMKEETRDLYSKL 130

Query: 132 KEKGKRSSEHIQRIDRDVSGTLRKHIFFRDRYGTKQRELLHILLAYEEYNPEVGYCRDLS 191  
K + + S I++ID DV+ T R HI FRDRYG KQ+ L H+L AY YN EVGYC+ +S  
Sbjct: 131 KHRARGCSPDIRQIDLDVNRTFRDHIMFRDRYGVKQQLFHVLAAYSIYNTEVGYCQGMS 190

Query: 192 HIAALFLLYLPEEDAFWALVQLLASERHSLQGFHSPNGGTVOQLDQDQEHVVATSQPKTM 251  
I AL L+Y+ EEDAFWALV+L + +H++ GF + Q+ E ++ K

Sbjct: 191 QITALLMYMNEEDAFWALVKLFSGPKHAMHGFFVQGFPKLLRFQEHHEKILNKFLSKLK 250

Query: 252 GHQDKKDLGCQCSPGLCLIRILIDGISLGLTLRLWDVYLVEGEQALMPITRIAFKVQQR 311  
H D +++ + + +D L LR+WD+Y+ EGE+ L ++ K+ +K

Sbjct: 251 QHLDSQEIIYTSFYTMKWFFQCFLDRTPFTLNLRWDIYIFEGERVLTAMSYTILKLHKKH 310

Query: 312 LTKTSRCGPWFRCNRFVDTWARD----EDTVLKHRLASMKKLTRKQGDLPKPAK----P 363  
L K S F +T A+D +D V++ L+ SM +L R + DLP P K P

Sbjct: 311 LMKLS----MEELVEFFQETLAKDFFEDDFVIEQLQISMTELKRAKLDLPEPGKEDEYP 366

Query: 364 EQGSSASRPVPASRGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPCPGGAVRE 423  
++ P S G L G R G P SP + R + P

Sbjct: 367 KKPLGQLPELQSWG VHLSNGQSV--GRP-----SPLASGRRESGAPHRHEH 414

Query: 424 DTYPVGTQGVPSA 437  
+P G P A

Sbjct: 415 SPHPQSRTGTPERA 428

>g28703740 Hypothetical protein MGC51025 [Homo sapiens]  
Length = 250

Score = 235 bits (594), Expect = 2e-60  
Identities = 120/206 (58%), Positives = 146/206 (70%), Gaps = 5/206 (2%)

Query: 18 IIMKYEKGHRAGLPEDKGPKEF--RSYNNNVLDHGLIVHETELPPLTAREAKQIRREISRK 75  
II KYE+GHRAG D G + R Y NN LGIVHE ELP ++A E KQ R+E R

Sbjct: 19 IITKYEQGHRAAAVDLGHEQVDVRKYTN--LGIVHEMELPRVSALEVKQRKEKSRK 75

Query: 76 SKWVDMLGDWEKYKSSRKLIDRAYKGMPMNIRGPMWSVLLNTEEMKLKNPGRYQIMKEKG 135  
+KW ML DW KY+S++KL R YK +P+ +RG WS+LL+ + +K +NPG+Y++MKEKG

Sbjct: 76 NKWQKMLADWTKYRSTKKSQRVYKVIPLAVRGRAWSLLLDIDRIKSQNPGRYKVMKEKG 135

Query: 136 KRSSEHIQRIDRDVSGTLRKHIFFRDYGTQRELLHILLAYEEYNPEVGYCRDLSHIAA 195  
KRSS I I DVS TL+KH+ F R+G KQ+EL IL+AY YNPEVGY RDLS I A

Sbjct: 136 KRSSRIIHCIQLDVSHTLQKHMMFIQRFVGVKQELCDILVAYSAYNPEVGYHRDLRITA 195

Query: 196 LFLLYLPEEDAFWALVQLLASERHSL 221  
+ LL LPEED FWAL QLLA ERHSL

Sbjct: 196 ILLLCLPEEDVFWALTQLLAGERHSL 221

Database: genpept136

Posted date: Jul 31, 2003 9:27 AM

Number of letters in database: 449,659,834

Number of sequences in database: 1,453,555

Lambda	K	H
0.319	0.136	0.436

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 550686865

Number of Sequences: 1453555

Number of extensions: 25993291

Number of successful extensions: 86626

Number of sequences better than 10.0: 846

Number of HSP's better than 10.0 without gapping: 199

Number of HSP's successfully gapped in prelim test: 682

Number of HSP's that attempted gapping in prelim test: 82213

Number of HSP's gapped (non-prelim): 2853  
length of query: 549  
length of database: 449,659,834  
effective HSP length: 54  
effective length of query: 495  
effective length of database: 371,167,864  
effective search space: 183728092680  
effective search space used: 183728092680  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.8 bits)  
X3: 64 (24.9 bits)  
S1: 41 (21.7 bits)

[Graphical Viewer](#)

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Submit sequences to:

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